

Result No.	Query			DB	ID	Description
	Match	Score	Length			
1	85.6	2799	620	11	O70550	mus musculus
2	78.8	2576.5	623	11	O88560	mus musculus
3	51.1	1672.5	619	4	Q9Y2P4	homo sapien
4	44.2	1452	690	4	Q9Y2P5	homo sapien
5	42.2	1379	662	11	O88694	mus musculus
6	41.7	1365	611	11	Q9ES38	mus musculus
7	40.6	1327.5	614	11	O88561	rattus norv
8	32.1	1051	671	5	Q9W1V9	mus musculus
9	31.4	1025	661	5	Q9W1V8	rosophila
10	30.1	983.5	690	5	Q9WVK1	rosophila
11	29.3	958	650	5	Q19878	rosophila
12	29.1	953	608	2	Q9H2V4	caenorhabdi
13	28.9	944	597	2	O05307	pseudomonas
14	28.6	937	641	4	O95186	mycobacteri
15	28.6	936	655	5	Q18916	homo sapien
16	28.4	927.5	506	11	O88562	mus musculus
17	27.9	913.5	643	3	O42633	cochliobolu
18	23.7	774.5	669	3	O60021	saccharomyc
19	12.2	398.5	502	2	O53551	mycobacteri

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Db 121 WLGLLVKLGCPMACLNINIRAKSLLHCFQCCGAKVLLASPDLOEAEEALPTLKDAVSFV 180
QY 181 YVSRNTDGDIDSLDKVDESTEPIESWSEVTFSTPALYIYTSGTGLPKAMITHQ 240
Db 181 YVSRNTDGDIDSLDKVDESTEPIESWSEVTFSTPALYIYTSGTGLPKAMITHQ 240
QY 241 RIWYGTGLFVSGLKADDDV-IYITLPHYSAALLIGHGCIIVAGATLALR-TKFSASQFW 300
Db 241 RIWYGTGLFVSGLKADDDV-IYITLPHYSAALLIGHGCIIVAGATLALR-TKFSASQFW 300
QY 301 CRKYNVTVIQYIGELLRYLNCSPQKPNDRDHKVRALNGLRGDVMRQVFRFGDICIYE 360
Db 301 CRKYNVTVIQYIGELLRYLNCSPQKPNDRDHKVRALNGLRGDVMRQVFRFGDICIYE 360
QY 361 FYAATGEGNIGFMYARKVAGVGRVNYLQKKIITDLYIKYDVEKDEPVRDENGVCVRV 420
Db 361 FYAATGEGNIGFMYARKVAGVGRVNYLQKKIITDLYIKYDVEKDEPVRDENGVCVRV 420
QY 421 EVGLLVCKITQITLTPFNGYAGAKAQTEKKKLRDVFVKKGLDYFNNSGDLMLMDRENFIYF 480
Db 421 EVGLLVCKITQITLTPFNGYAGAKAQTEKKKLRDVFVKKGLDYFNNSGDLMLMDRENFIYF 480
QY 481 VGDTRFKNGENVAATEVADIVGLVDFVQVBNYGVHPDHEGRIGMASIKMKENHEF 540
Db 481 VGDTRFKNGENVAATEVADIVGLVDFVQVBNYGVHPDHEGRIGMASIKMKENHEF 540
QY 541 KLFOHIAEYLPYARPRFLRIODTITGTGFKHKMTLVEEGFNPAVVKDALYFLDDTAK 600
Db 541 KLFOHIAEYLPYARPRFLRIODTITGTGFKHKMTLVEEGFNPAVVKDALYFLDDTAK 600
QY 601 MYVPMTEIYNAISAKTLK 620
Db 601 TEVPMTEIYNAISAKTLK 620

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RESULT 2

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O88560 PRELIMINARY; PRT; 623 AA.
ID O88560
AC O88560
DT 01-NOV-1998 (TREMREL. 08, Created)
DT 01-NOV-1998 (TREMREL. 08, Last sequence update)
DT 01-MAY-2000 (TREMREL. 13, Last annotation update)
DE FATTY ACID TRANSPORT PROTEIN 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98337965; PubMed=9671728;
RA Hirsch D., Stahl A., Lodish H.F.;
RT "A family of fatty acid transporters conserved from mycobacterium to
man."
RL EMBL; AF072757; AAC40186.1;
DR InterPro: IPR000873;
DR Pfam: PF00501; AMP-binding; 1.
DR PROSITE; PS00455; AMP_BINDING; 1.
SQ SEQUENCE 623 AA; 70594 MW; 81CC62831384E127 CRC64;

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Query Match 78.8%; Score 2576.5; DB 11; Length 623;
 Best Local Similarity 77.4%; Pred. No. 1.4e-185;
 Matches 482; Conservative 54; Mismatches 84; Indels 3; Gaps 3;

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QY 1 MLSAIYTVL-AGLLFLPLLVNLCPPYFQDYGIVFLKVAAGVRRVSRVQRRPARTILRAF 60
Db 1 MLPVYITGLAGLLPLLLTCCCPYLLQDVYFLRLANMARVSRVQRRPARTILRAF 60
QY 61 EKARQTPHPKPFLLFRDRETLTYAQVDRRSNQVARRALHDHGLRGQDCVALLMGNEPAYVW 120
Db 61 EQARKTPHPKPFLLFRDRETLTYAQVDRRSNQVARRALHDHGLRGQDCVALLMGNEPAYVW 120

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QY 121 WLGLLVKLGCPMACLNINIRAKSLLHCFQCCGAKVLLVSPLOAAVEEILPSLKDDVSIV 180
Db 121 WLGLLVKLGCPMACLNINIRAKSLLHCFQCCGAKVLLASPDLOEAEEALPTLKDAVSFV 180
QY 181 YVSRNTDGDIDSLDKVDESTEPIESWSEVTFSTPALYIYTSGTGLPKAMITHQ 240
Db 181 YVSRNTDGDIDSLDKVDESTEPIESWSEVTFSTPALYIYTSGTGLPKAMITHQ 240
QY 241 RIWYGTGLFVSGLKADDDV-IYITLPHYSAALLIGHGCIIVAGATLALR-TKFSASQFW 298
Db 241 RIWYGTGLFVSGLKADDDV-IYITLPHYSAALLIGHGCIIVAGATLALR-TKFSASQFW 298
QY 298 DD-CRKYNVTVIQYIGELLRYLNCSPQKPNDRDHKVRALNGLRGDVMRQVFRFGDICI 357
Db 298 DD-CRKYNVTVIQYIGELLRYLNCSPQKPNDRDHKVRALNGLRGDVMRQVFRFGDICI 357
QY 357 IYEFYATGEGNIGFMYARKVAGVGRVNYLQKKIITDLYIKYDVEKDEPVRDENGVCVRV 417
Db 357 IYEFYATGEGNIGFMYARKVAGVGRVNYLQKKIITDLYIKYDVEKDEPVRDENGVCVRV 417
QY 417 YVEFYASTGEGNIGFMYARKVAGVGRVNYLQKKIITDLYIKYDVEKDEPVRDENGVCVRV 420
Db 417 YVEFYASTGEGNIGFMYARKVAGVGRVNYLQKKIITDLYIKYDVEKDEPVRDENGVCVRV 420
QY 420 PKGEVGLLVCKITQITLTPFNGYAGAKAQTEKKKLRDVFVKKGLDYFNNSGDLMLMDRENFIYF 477
Db 420 PKGEVGLLVCKITQITLTPFNGYAGAKAQTEKKKLRDVFVKKGLDYFNNSGDLMLMDRENFIYF 477
QY 477 HDRVGDTRFKNGENVAATEVADIVGLVDFVQVBNYGVHPDHEGRIGMASIKMKENHEF 537
Db 477 HDRVGDTRFKNGENVAATEVADIVGLVDFVQVBNYGVHPDHEGRIGMASIKMKENHEF 537
QY 537 DKKLFQHIAEYLPYARPRFLRIODTITGTGFKHKMTLVEEGFNPAVVKDALYFLDD 597
Db 537 DKKLFQHIAEYLPYARPRFLRIODTITGTGFKHKMTLVEEGFNPAVVKDALYFLDD 597
QY 597 TAKMYVPMTEIYNAISAKTLK 620
Db 597 TAKMYVPMTEIYNAISAKTLK 620
QY 601 AETFPVPMTEIYNAISAKTLK 623
Db 601 AETFPVPMTEIYNAISAKTLK 623

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RESULT 3

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Q9Y2P4 PRELIMINARY; PRT; 619 AA.
ID Q9Y2P4
AC Q9Y2P4
DT 01-NOV-1999 (TREMREL. 12, Created)
DT 01-NOV-1999 (TREMREL. 12, Last sequence update)
DT 01-MAR-2001 (TREMREL. 16, Last annotation update)
DE VERY LONG-CHAIN ACYL-COA SYNTHETASE HOMOLOG 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Steinberg S.J., Watkins P.A.;
RT "Human Very Long-Chain Acyl-CoA Synthetase Homolog 1."
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF064254; AAD29443.1;
DR InterPro: IPR000873;
DR Pfam: PF00501; AMP-binding; 1.
DR PROSITE; PS00455; AMP_BINDING; 1.
SQ SEQUENCE 619 AA; 70111 MW; 20264CE3FBB44FF5 CRC64;

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Query Match 51.1%; Score 1672.5; DB 4; Length 619;
 Best Local Similarity 50.7%; Pred. No. 1.5e-117;
 Matches 315; Conservative 116; Mismatches 187; Indels 3; Gaps 3;

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QY 1 MLSAIYTVL-AGLLFLPLLVNLCPPYFQDYGIVFLKVAAGVRRVSRVQRRPARTILRAF 59
Db 1 MLLSMLTVLIGAGMVVLFHQLKLLFPYFDDDFWFLVKVLLIIRLKKYKRGELVTLDFK 60
QY 60 LEKARQTPHPKPFLLFRDRETLTYAQVDRRSNQVARRALHDHGLRGQDCVALLMGNEPAYVW 119
Db 60 LSHAKRQPRKPFLLFRDRETLTYAQVDRRSNQVARRALHDHGLRGQDCVALLMGNEPAYVW 120

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QY 120 LNLGLVKLGACACLNINIRAKSLHHCFOCCGAKVLLVSPQLAAVEEILPSLKDDVSI 179
Db 121 VWFGLAKLGCVAFNLNINIRAKSLHHCFOCCGAKVLLVSPQLAAVEEILPSLKDDVSI 179
QY 180 YYVSRSTNTDGDIDFSLDKVDEVSTETIPESWRSEVTFSTPALYIYSGTGLPKAAAMITH 239
Db 180 WGM-KDSVPQGVISLKEKLSSTPDEVPVRSHVSVLLSKTCLYIFSGTGLPKAAVISO 238
QY 240 QRIWYGTGLTFVSLKADDDVYITLFPYHSAALLIGHGIVAGATLALTRKFSASQFWD 299
Db 239 LQVLRGSAVLWAFGCTAHDIVYITLPLVHSSAAILGISGVELGATCVLKKKFSASQFWS 298
QY 300 DCRKYNVTQYIGELLRLYLCNSPQPNDRDHKRLVRLALNGRLGDMVROFVKREGDICIY 359
Db 299 DCKKYDVTQYIGELLRLYLCNSPQPNDRDHKRLVRLALNGRLGDMVROFVKREGDICIY 358
QY 360 EYVAAETGNTGFNMYARKVAGVGRVNYLQKIITYDLIKYDEKDEPFVRDENGICYVRPK 419
Db 359 ELYAAETESSISFMYTGRIGARTNLVYKLLSTFDLIKYDQKDEPMNEQGWCIHVKK 418
QY 420 GEVGLLVCKITQITLTPNGVAGAKAOTEKKLRDVFVKKGLDLYNSGDLMLVMDHNFYFHD 479
Db 419 GEPGLLSIRVNAKNPFGVAGPYKHKDKLLCDVFKKGDVYLTGDLIVQDDNFYFWD 478
QY 480 RVGDTFRWKGENVATTEVADTVGLDVFQVGVVYGVHVPDHEGRIGMASIKMKENHEFDG 539
Db 479 RTGDTFRWKGENVATTEVADTVGLDVFQVGVVYGVHVPDHEGRIGMASIKMKENHEFDG 538
QY 540 KLFQHIADYLPYARPRELRIODTTEITGTFKHKRMTLVEEGFNPAVTKDALYFLDDTFA 599
Db 539 EKVEQVWTFPLPAYACPRELRIODTTEITGTFKHKRMTLVEEGFNPAVTKDALYFLDDTFA 598
QY 600 KMYPMTEIDIYNAISAKTLKL 620
Db 599 KSYVLLTRELVDQIMLGEIKL 619

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RESULT 4

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QY2P5 ID QY2P5 PRELIMINARY; PRT; 690 AA.
AC QY2P5;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE VERY LONG-CHAIN ACYL-COA SYNTHETASE HOMOLOG 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Steinberg S.J., Wang S.J., Watkins P.A.;
RT "Human Very Long-Chain Acyl-CoA Synthetase Homolog 2.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF064255; AAD29444.1;
DR InterPro; IPR000873;
DR Pfam; PF00501; AMP-binding; 1.
DR PROSITE; PS00455; AMP_BINDING; 1.
SQ SEQUENCE 690 AA; 75384 MW; 011313424D794546 CRC64;

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Query Match

Best Local Similarity 44.4%; Score 1452; DB 4; Length 690;

Matches 279; Conservative 127; Mismatches 193; Indels 20; Gaps 4;

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QY 11 GLFLFLPLVNLCCPYFFDQIGVFLKVAAGVRRVRSYGGRRPARTILRAFLEKARQTPHKP 70
Db 83 GLRWLP-----ADVFLAKILHLKIRCLSRQPPDFVDAFERARRAQPGRA 131
QY 71 FLFLRDE---TLTYAQVRRSNQARALHDHIG-----LRQGDCAVLLMGNEPAY--VWLW 121
Db 132 LLVWTGPGAGSVTFGELDARACQAALWALKAEGLDGPASCAGEPTALLVLAQVAPLCMW 191

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QY 122 LGLVKGACACLNINIRAKSLHHCFOCCGAKVLLVSPQLAAVEEILPSLKDDVSIY 181
Db 192 LGLAKLGCTAPAINPHGRGMPLAHSLVSSGARVLVVDPLRESLEEILPKLAENIRCFY 251
QY 182 VSRSTNTDGDIDFSLDKVDEVSTETIPESWRSEVTFSTPALYIYSGTGLPKAAAMITHOR 241
Db 252 LSHTSPTFGVAGALGAALDAAPSHVPADLRAGITWRSFALFIYSGTGLPKPALITHER 311
QY 242 TWYGTGLTFVSLKADDDVYITLFPYHSAALLIGHGIVAGATLALTRKFSASQFWD 301
Db 312 VLQMSKMLSLSGATADDVVYTVPLVHYVGLVGLGCLDGLGATCVLAPKESTSCFWD 371
QY 302 RKNYNTVQYIGELLRLYLCNSPQPNDRDHKRLVRLALNGRLGDMVROFVKREGDICIYEF 361
Db 372 RQHGVTYVQYIGELLRLYLCNIPQOPEDRTHVRLAMGLRADVWETFOQRFPIRIWEV 431
QY 362 YAAETGNTGFNMYARKVAGVGRVNYLQKIITYDLIKYDEKDEPFVRDENGICYVRPK 421
Db 432 YGSTEGLNGLVNYVGRGALGMSCLRLMSLFFELVDFDMEAAEPVRDNOGFCIPVLGE 491
QY 422 VGLLVCKITQITLTPNGVAGAKAOTEKKLRDVFVKKGLDLYNSGDLMLVMDHNFYFHD 481
Db 492 PGLLLTKVVSQOPFVYGRPRELSEKRLVNRVSGDYYNTGDLVLRDREGFLYFRDL 551
QY 482 GDTFRWKGENVATTEVADTVGLDVFQVGVVYGVHVPDHEGRIGMASIKMKENHEFDGKK 541
Db 552 GDTFRWKGENVSTHEVEGLVSQLDVFLOQVNVYGVCPGCEGKVGMAAQLAPGQTDFGEK 611
QY 542 LFOHIADYLPYARPRELRIODTTEITGTFKHKRMTLVEEGFNPAVTKDALYFLDDTAKM 601
Db 612 LYQHVRAWLPAYATPHFIRIQDAMEVTSTFKMLKTRLVREGFNVGIVDPLFVLDRQA 671
QY 602 YVPMTEIDIYNAISAKTLKL 620
Db 672 FRPLTAEMYQAVCEGTWRL 690

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RESULT 5

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O88694 ID O88694 PRELIMINARY; PRT; 662 AA.
AC O88694;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-AUG-1999 (Tremblrel. 11, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE FATTY ACID TRANSPORT PROTEIN 5 PRECURSOR (FATP5) (LONG-CHAIN FATTY
DE ACID TRANSPORT PROTEIN 5) (VERY-LONG-CHAIN ACYL-COA SYNTHETASE RELATED
DE PROTEIN)
GN SLIC27A5 OR VLACS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98337965; PubMed=9671728;
RA Hirsch D., Stahl A., Lodish H.F.;
RT "A family of fatty acid transporters conserved from mycobacterium to
RT man.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:8625-8629(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE=LIVER;
RX MEDLINE=98308102; PubMed=9642112;
RA Berger J., Truppe C., Neumann H., Forss-Petter S.;
RT "A novel relative of the very-long-chain acyl-CoA synthetase and fatty
RT acid transporter protein genes with a distinct expression pattern.";
RL Biochem. Biophys. Res. Commun. 247:255-260(1998).
CC -1- FUNCTION: INVOLVED IN TRANSLLOCATION OF LONG-CHAIN FATTY ACIDS
CC ACROSS THE PLASMA MEMBRANE. MAY PLAY A PIVOTAL ROLE IN REGULATING
CC AVAILABLE LONG-CHAIN FATTY ACID SUBSTRATES FROM EXOGENOUS SOURCES
CC IN TISSUES UNDERGOING HIGH LEVELS OF BETA-OXIDATION OR
CC TRIGLYCERIDE SYNTHESIS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. PLASMA MEMBRANE.

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CC -1- TISSUE SPECIFICITY: LIVER, BUT NOT IN FETAL LIVER. LOW LEVELS IN
 CC BRAIN, LUNG, TESTES, SPLEEN, AND SKELETAL MUSCLE.
 CC -1- SIMILARITY: TO OTHER ENZYMES WHICH ACT VIA AN ATP-DEPENDENT
 CC COVALENT BINDING OF AMP TO THEIR SUBSTRATE.
 DR EMBL; AF072760; AAC40189.1; -.
 DR EMBL; AJ223959; CAAL1688.1; ALT_INIT.
 DR MGI; MGI:1347100; SLC27A5.
 DR InterPro; IPR000873; -.
 DR Pfam; PF00501; AMP-binding; 1.
 DR PROSITE; PS00455; AMP-binding; 1.
 KW Glycoprotein; Lipid transport; Transmembrane; Signal; Transport.
 FT SIGNAL 1 26 POTENTIAL.
 FT CHAIN 27 662 FATTY ACID TRANSPORT PROTEIN 5.
 FT TRANSMEM 28 48 POTENTIAL.
 FT TRANSMEM 156 176 POTENTIAL.
 FT TRANSMEM 312 332 POTENTIAL.
 FT CARBOHYD 533 533 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CONFLICT 1 1 M -> MGIWKKLTLLLLLLVGLGQPPWPRAM (IN
 REF. 2).
 FT CONFLICT 61 61 K -> I (IN REF. 2).
 FT CONFLICT 381 381 T -> N (IN REF. 2).
 FT CONFLICT 541 541 C -> S (IN REF. 2).
 FT CONFLICT 661 661 N -> K (IN REF. 2).
 SQ SEQUENCE 662 AA; 73251 MW; 1D7BAFE29F6D2712 CRC64;

Query Match 42.2%; Score 1379; DB 11; Length 662;
 Best Local Similarity 42.0%; Pred. No. 2.2e-95;
 Matches 264; Conservative 136; Mismatches 218; Indels 10; Gaps 3;

QY 2 LSATYIVLAGLLPLLLVNLCCPFYFQDGYFLKVAAGRRVRSYQORPARTILRAFLE 61
 DB 36 LSLVGAALT-LFLLPLPPGLKHLKDVAFKMLFYGLKFRRLNKKHPPETFDVALER 94
 QY 62 KAROTHPKPELL---FRDETLTYAQRDRSRNOVARALHDHL-----GLRQDCVALLMG 112
 DB 95 QALAWPDRVALVCTGSESSITNSQLDARSQAAVLAKKLDAVIONTRDAALILVLP 154
 QY 113 NEPAYVWLGLVGLKGCAMACLNINRAKSLHCFQCCAKVLLVSPLOAAVEILPSL 172
 DB 155 KTISALSVFLGAKLGPVAMINPHSRGMPLLSHVSRSGLVLDVDPDQENLEELPKL 214
 QY 173 KDDVSYIYVSRTSNTDIDSLDKVDVSTPEIPESRSEVTFSPALYIYTSGTGLP 232
 DB 215 LAENICFYLGHSPPGVEALCASIDAAPSDVPASLRATKWKSPALFIYTSGTGLP 274
 QY 233 KAAMITHQRIWYGTGLTFVSGLKADDDVYITLFFYHSAALLIGIHGCIIVAGTALRTKF 292
 DB 275 KPAILSHERVIOQSVNLSPFCGRADDDVYDVLPLXHTIGLVGLGCLQVATCVLAPKF 334
 QY 293 SASQFDDCKRYNTYIYIGELLRYLCSPOKPNDRDHKVRALGNGLRGDVRQFVKR 352
 DB 335 SASRFAECRQHGVTVILYVGEILRYLNVPEQPEKIHIVRLAMGTGLRANVKNFOOR 394
 QY 353 FGDCIYEFYAATEGNIGFMNARKVGAAGRVNLYLQKKIITVDLIKYDVEKDEPVRDENG 412
 DB 395 FGPRLWEFGSTEGNVLNMGVCHGAGVGRISILRMLTPPELVQFDIETAEPLRDKG 454
 QY 413 YCVRVPKGEVGLLVCKITQITLTPFNGYAGAKAQTEKKLRDVFKKGDLXFNPSGDLMLVD 472
 DB 455 FCIPVEPGKPLLTKVRKNOPPLGYRGSAENRKLAVNRVVGDLFYENTGDLVTLQDE 514
 QY 473 NFIFYHDRVGDTRFKGENVATTEVADTVGLVDVFOEVNNGVHYVDPDHGRIGMASIRMK 532
 DB 515 GFYFQDRLDGDTFRWKGENVSTGEVCEVLSSDLFEVNNGVYGPVPGCGEKVGAALKVA 574
 QY 533 ENHEFGKGLFOHADIYLPYSAPRFLRIQDTIETGTFKHKWTLVEEGFNPAVTKDAL 592
 DB 575 PGKTFGQKLYQHVRSWLPAYATPHFIRIQDSLEITNTKLYKSLRVREGDFVGIADPL 634
 QY 593 YFLDDTAKMVPMTEDIYNAISAKTLK 620
 DB 635 YILDNKAQTFRSLMPDVOYQAVCEGTWNL 662

RESULT 6

Q9ES38 PRELIMINARY; PRT; 690 AA.
 ID Q9ES38
 AC Q9ES38;
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
 DE BILE ACID COA LIGASE
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPRAIN-SPRAQUE-DAWLEY;
 RA Falany C.N., Xie X., Wheeler J., Wang J., Barnes S.;
 RL "Molecular cloning and expression of rat liver bile acid CoA ligase."
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF242189; AAG09770.1; -.
 KW Ligase.
 SQ SEQUENCE 690 AA; 76265 MW; D5BEB8317758DA59 CRC64;

Query Match 41.7%; Score 1365; DB 11; Length 690;
 Best Local Similarity 41.3%; Pred. No. 2.6e-94;
 Matches 267; Conservative 134; Mismatches 212; Indels 34; Gaps 5;

QY 8 VLAGLLFL-----PLLNVNLCCP-----YFFQDIGYFLKVAAGRR 42
 DB 44 VLLGLAFGRWISWIPHWLSLAAALTLSPRPPELRLWHLKDVAFKLLFYGLN 103
 QY 43 VRSYQRRPARTILRAFLEKARQTPHPFFLLFRDE---TLTYAQVDRRSNQVARALHDHL 99
 DB 104 LRRRLRHPPELFVDALDAQQAARPDQVALVCTGSECSITNRELNAKACAAWALKAKL 163
 QY 100 --GLRQD---CVALLMGNPEYVWLWGLVGLKGCAMACLNINRAKSLHCFQCCAK 153
 DB 164 KEATIQEDKGATILVLPKSIKLSALSVFLGAKLGPVAMINPHSRGMPLLSHVSRSGLS 223
 QY 154 VLLVSPLELQAAVEELPSLKDDVSYIYVSRTSNTDIDSLDKVDVSTPEIPESRSE 213
 DB 224 VLIIVDPDQENLEELVPLKLAENIRCFYLGHSPTPGVEALGAALDAAPSDVPKALRAN 283
 QY 214 VTFSTPALYIYTSGTGLPKAAMITHQRIWYGTGLTFVSGLKADDDVYITLFFYHSAALL 273
 DB 284 IKWKSFAIFIYTSGTGLPKPAILSHERVIOQSVNLSPFCGRADDDVYDVLPLXHTIGLV 343
 QY 274 IGIHGCIVAGATLALRTKFSASQFDDCKRYNTYIYIGELLRYLCSPOKPNDRDHV 333
 DB 344 LGVLGCLQGLGATCVLAPKFSASRYWAECSQYSVTVVLVYGEVLRKLVNPGQPEDKHTV 403
 QY 334 RLALGNGLRGDVRQFVKRFGDCIYEFYAATEGNIGFMNARKVGAAGRVNLYLQKKIIT 393
 DB 404 RFALGNGLRADVWENFQQRFGPIQIWEILYSGTEGNGLMNVYVGHGAVGKTSFCFIRMLTP 463
 QY 394 YDLIKYDVEKDEPVRDENGICVVRPKGEVGLLVCKITQITLTPFNGYAGAKAQTEKKLRDV 453
 DB 464 LELVQFDIETAEPRDKQGFICPVEYKPGKPLLTKVRKNOPPLGYRGSAENRKLAVN 523
 QY 454 FKKGDLVFNSGDLMLVDHENFIYFPHDRVGDTRFKGENVATTEVADTVGLVDVFOEVN 513
 DB 524 RQVGLDIYNTGDVLLALQDEGFFYFRDLRGDTRFKGENVSTREVEGVLSILDFLEEVN 583
 QY 514 GVHPDHEGRIGMASIRKMKENHEPDKGLKQHIADYLPYSAPRFLRIQDTIETGTFKH 573
 DB 584 GVTVPCEGKGVGAALKAPGKTFDGQKLYQHVRSWLPAYATPHFIRIQDSLEITNTYKL 643
 QY 574 RKMTLVVEEGFNPAVTKDALYFLDDTAKMVPMTEDIYNAISAKTLK 620
 DB 644 VKSQLAREGDFGVGIADPLYILDNKAETFRSLMPDVOYQAVCEGTWNL 690

388	QY	OKKIITVYDLIKYDEKDEPVRDENGICVRVPKGEVGLLVCKITQLTPFNFGYAGAKAQTEK	441
389	Db	IKKIIITVYDLIKYDEKDEPVRDENGICVRVPKGEVGLLVCKITQLTPFNFGYAGAKAQTEK	442
390	Db	IKKIIITVYDLIKYDEKDEPVRDENGICVRVPKGEVGLLVCKITQLTPFNFGYAGAKAQTEK	443
391	QY	KKLRDVKPKGDLFNSGDLILMDVHFNFIYFHDVRGDTFRKWKGNVATTEVADTVGLVDVF	507
392	Db	KKLRDVKPKGDLFNSGDLILMDVHFNFIYFHDVRGDTFRKWKGNVATTEVADTVGLVDVF	508
393	QY	KKLRDVKPKGDLFNSGDLILMDVHFNFIYFHDVRGDTFRKWKGNVATTEVADTVGLVDVF	509
394	Db	KKLRDVKPKGDLFNSGDLILMDVHFNFIYFHDVRGDTFRKWKGNVATTEVADTVGLVDVF	510
395	QY	QEVNIVYGVHVDHHEGRIGMASIKMKENHEFDGKKLFQHTADYLPSPYRFRFLQDITIEI	567
396	Db	QEVNIVYGVHVDHHEGRIGMASIKMKENHEFDGKKLFQHTADYLPSPYRFRFLQDITIEI	568
397	QY	QEVNIVYGVHVDHHEGRIGMASIKMKENHEFDGKKLFQHTADYLPSPYRFRFLQDITIEI	569
398	Db	QEVNIVYGVHVDHHEGRIGMASIKMKENHEFDGKKLFQHTADYLPSPYRFRFLQDITIEI	570
399	QY	TGTFKHKRMTLVEEGNPNPAVIKDALYFLDDTAKWYPMPTEDIYNAISAKYTKL	620
400	Db	TGTFKHKRMTLVEEGNPNPAVIKDALYFLDDTAKWYPMPTEDIYNAISAKYTKL	621
401	QY	TGTFKHKRMTLVEEGNPNPAVIKDALYFLDDTAKWYPMPTEDIYNAISAKYTKL	622
402	Db	TGTFKHKRMTLVEEGNPNPAVIKDALYFLDDTAKWYPMPTEDIYNAISAKYTKL	623
403	QY	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
404	Db	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
405	QY	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
406	Db	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
407	QY	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
408	Db	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
409	QY	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
410	Db	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
411	QY	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
412	Db	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
413	QY	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
414	Db	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
415	QY	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
416	Db	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
417	QY	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
418	Db	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
419	QY	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
420	Db	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
421	QY	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
422	Db	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
423	QY	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
424	Db	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
425	QY	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
426	Db	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
427	QY	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
428	Db	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
429	QY	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
430	Db	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
431	QY	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
432	Db	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
433	QY	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
434	Db	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
435	QY	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
436	Db	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
437	QY	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
438	Db	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
439	QY	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
440	Db	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
441	QY	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
442	Db	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
443	QY	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
444	Db	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
445	QY	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
446	Db	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
447	QY	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
448	Db	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
449	QY	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
450	Db	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
451	QY	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
452	Db	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
453	QY	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
454	Db	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
455	QY	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
456	Db	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
457	QY	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
458	Db	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
459	QY	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
460	Db	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
461	QY	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
462	Db	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
463	QY	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
464	Db	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
465	QY	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
466	Db	Q9W1V9 PRELIMINARY; PRT; 671 AA.	
467	QY	Q9W1V9 PRELIMINARY; PRT; 671 AA.	


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Db 374 LRLMGLRQWQVFRFGIPHGEIYGATEGNSNLININRVAIGFVFPVYSSLY 433
QY 393 TYDLIKYDEKDFPVRDENGVCYVRPKGEVGLLVCKI---TOLTPEYAGAKAOTEKKK 449
Db 434 PQVQLRDEYTGELLKDSRGHCIRCPQAGLGVKVDARRAVSAPHGAD-KGASEQKL 492
QY 450 LRDFVFKGDDLYFNSSGDLMLVMDHNFYIFHDRVGDTPFRWGENVATTEV----ADTVGLVD 505
Db 493 LRVNFTSGDVFNFSGDMVVRDILGYFYFKDRTGDTFRWGENVATTEV---ADTVGLVD 505
QY 506 FVQEVNRYGVHVPDHPGEMASIKMKENHEPDGKLLFQHIADYLPYSYARFRLRIQDTY 565
Db 553 CV-----YGVQIHPVHGKAGMAI-VDPERKVDMDYLSVVLGRSGLPYARPLFRLDEI 607
QY 566 EITGTFKHKMTLVGEGFNPVAVIKDALYFLDDTAKMVPWMTD 608
Db 608 PRATEKLAKRELAKAYDIGQSDPIYINRDG-IYRPLSQE 649

RESULT 10
Q9WKU1 ID Q9WKU1 PRELIMINARY; PRT; 690 AA.
AC Q9WKU1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 16, Last annotation update)
DE CG7400 PROTEIN.
GN FATP OR CG7400.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.I., Benos P.V., Beriman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Chery J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleib J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reibert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,

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RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195 (2000).
DR EMBL; AE003629; AAF52969.1; -.
DR FlyBase; FBgn0021953; Fatp.
DR InterPro; IPR000873; -.
DR Pfam; PF00501; AMP-binding.1.
DR PROSITE; PS00455; AMP-BINDING; 1.
SQ SEQUENCE 690 AA; 77541 MW; 3A1B7CCDB104060B CRC64;

Query Match 30.1%; Score 983.5; DB 5; Length 690;
Best Local Similarity 37.4%; Pred. No. 1.4e-65;
Matches 216; Conservative 108; Mismatches 222; Indels 31; Gaps 11;

QY 54 TILRAFLEKARQTHPKFLLPRDETLYAQVDRRSNOVARALHDLGRQDCVALLMGN 113
Db 133 TVADVFERNVOAHPDKVAVVSETQRTFRQVNEHANKVANVLAQ-GYKKGVVALLLEN 191
QY 114 EPAYVWLWGLVGLKGCAMACLNINIRAKSLHCFQCCGAKVLLVSPLOAAVEILLPSLK 173
Db 192 RAEYVATWGLSKIGVITPLINTNLRGPSLLHSTVAHCSALIIYGEDFLCAVTDVAKDLP 251
QY 174 KDDVSIYVSRSTNDSIDGDFLDKXDE----VSTEPIFESWRSEVTFSTPALXIYTSGT 229
Db 252 A-NLTFLQFNENNNSSETEKNIPQAKNLNALLTTASVEKPNKTQVNHDKLVIYTSGT 310
QY 230 GLPKAAMTHOR-IWYGTGLTFYSGLKADDVYITLFFYSAALLIGIHCIVAGATLAL 288
Db 311 GLPKAAVISHSRYLFIAGIHYTMGFEEDIFVTPLPYTAGGIMCGOSVLFSGTSTVI 370
QY 289 RTKESQFQWDCRKYNTVYQIYIGELLRYLNCSPQKN--DRDHKVRALGALNGLRGDVW 346
Db 371 RKKFSASNYFADCAKYNATV-----TTPSEYDQKHVRVLFVFGNGLRQIWI 416
QY 347 RQVVRGDICTIYEFYAATEGNIGFMNRYKVGAVGRVNYLQKKIITDILIKYDVEKDEP 406
Db 417 PQFVQFENIAKVGFEYGAEGNANIMHNDVTGAIGFVSRIPLKVIPIISIRADPDTEP 476
QY 407 VRDENGCVVRPKGEVGLLVCKITQLTLP---FNGYAGAKAQTETKKLRDVFYKGLDYFNS 463
Db 477 IDRNGLQCLCAPNEPGVFIKIVKGNPSREFIYGVDEKA-SAKKIVKDYFKHGDMAFTS 535
QY 464 GDLMLVDHNFYIFHDRVGDTPFRWGENVATTEVADTVGLVDFVQEVNRYGVHVPDHPG 523
Db 536 GDLMLVADEKLYFKDRTGDTFRWGENVSTSEVAQVSNVAGYKDTVYGVITPTEGR 595
QY 524 IGASIKMKENHEFDGKKLFQHIADYLPYSYARFRLRIQDTIETGTFKHKMTLVVEEGF 583
Db 596 AGMAIYDPE-RELDLDVFAASLAKVLPAYARPQIIRLLTKVDLTGTFKLRKVDLQKEG 654
QY 584 NPAVICKDALYFLDDTAK-MVPMPTEDITYNAISAKTLK 619
Db 655 DPNAIKDALY--QTSKGRYELLTPQYDQVQNEIR 689

RESULT 11
Q19878 ID Q19878 PRELIMINARY; PRT; 650 AA.
AC Q19878;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE FATTY ACID TRANSPORTER PROTEIN A (F28D1.9 PROTEIN).
GN F28D1.9.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Baynes C.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.

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CC -!- FUNCTION: INVOLVED IN TRANSLOCATION OF LONG-CHAIN FATTY ACIDS (BY
CC SIMILARITY).
CC -!- SIMILARITY: TO OTHER ENZYMES WHICH ACT VIA AN ATP-DEPENDENT
CC COVALENT BINDING OF AMP TO THEIR SUBSTRATE.
DR EMBL: Z70684; CAA94602.1; -.
DR WormPep; F28D1.9; CE05749.
DR InterPro; IPR000873; -.
DR Pfam; PF00501; AMP-binding; 1.
DR PROSITE; PS00455; AMP-binding; 1.
KW Glycoprotein; Lipid transport; Transmembrane; Transport.
FT TRANSMEM 23 43 POTENTIAL.
FT TRANSMEM 137 157 POTENTIAL.
FT TRANSMEM 286 306 POTENTIAL.
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 518 518 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 650 AA; 72759 MW; F2D16649EA13288A CRC64;

Query Match 29.3%; Score 958; DB 5; Length 650;
Best Local Similarity 38.5%; Pred. No. 1e-63;
Matches 222; Conservative 97; Mismatches 225; Indels 32; Gaps 15;

QY 59 FLEKARQTHKPKPL--LFRDELTITVAQVDRSRNOVARALHDLHGLRQDCVALLMGNEPA 116
DB 81 FLDIVKKNPKAMIDIEITNTTETAEFAHCNRYANYFQG-LGYRSGDVALYMSVSE 139
QY 117 YVWLGLVGLKGCAMACLNINRAKSLHLCFOCCGAKVLLVSPQLQ---AAVEEILPSL 172
DB 140 FVAWNLAKIGVVTAWINSNLRKQOLVHCITASKTAIITSVTONIMLDAIDQKL--F 197
QY 173 KDDVSIYVYVRSNTGDSFLDKVD-EVSTPEIPESRSEVTFSTPALYIYTSGLTGL 231
DB 198 DVGIEVYSGEPKNSGFKNLKLDQAQITTEP---KTLDIVDFKSLICFIYTSGLTGM 254
QY 232 PKAAMITHOR---IWYGTGLTFVSGLKADDDVITLPPVHSAALLIGHGCIIVAGATLAL 288
DB 255 PKAAVWKHFRIYSIAVGAAKSP--GIRPSDRMVSNPIVHTAAGILGVQALLGSSCVI 312
QY 289 RTKFSASQFDDCKRYNVTYQVIGELLYLNCSPKPNDRDHKVRALGNLGRDGVWRQ 348
DB 313 RKKFSASNFRDCKVYDCTVSQVIGETICRYLLAQPVVEESRHRMLLVGNLRAEIQWP 372
QY 349 FVKRFQDICIYEFAATEGNIGMNYARKVAVG--RVNVLOKIIITYDLIKYDVEKDEP 406
DB 373 FVDRF-RVRIGELYSGTESSLVNIDGHVGCGLFPISLPKMKHPVRLIKVDVDTGEA 431
QY 407 VRDENGVCYVRPKGEVGLLVCKITQLTP---FNGYAGAKAQTEKKLRDVFKKGLDYFS 463
DB 432 IRSDGLCIACNPGESGAMVSTIRKNPLLLQFEGYLN-RKETNKKLIIRDVFAKGSCLFT 490
QY 464 GDLMDHNFYIFHDVGRVDFRWKGENVATTEVADTVGLVDFVQEVNYYGVHVPDHEGR 523
DB 491 GDLMDHNLGYVYFKDRTGDTFRWKGENVSTTEVEAILHPITGLSDATYVGVVEVPOREG 550
QY 524 IGMAIKMENHEFDGKKLFQH---IADYLPYSARPRFLRIQDTIETGTFFKHKMPL 578
DB 551 VGMASVVRVVSHEED-ETQPVHRVGARLASSLTSYAIPQFMRICODVEKGTGFKLVKTNL 609
QY 579 VEEGFNPVAKDALYFLDDTAKMVPMTEDIYNAL 614
DB 610 QRLGIMADP-SDSIYIYNSNRRNFVDFNDLRCKVS 644

RESULT 12
Q9HZV4 PRELIMINARY; PRT; 608 AA.
AC Q9HZV4
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE PROBABLE VERY-LONG-CHAIN ACYL-COA SYNTHETASE.
GN PA2893.
OS, Pseudomonas aeruginosa.

OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20437337; PubMed=10984043;
RX Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Huynhag W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL: AE004715; AAG06281.1; -.
DR InterPro; IPR000873; -.
DR Pfam; PF00501; AMP-binding; 1.
DR PROSITE; PS00455; AMP-BINDING; 1.
SQ SEQUENCE 608 AA; 67647 MW; D2E134AB8BAD4FF7 CRC64;

Query Match 29.1%; Score 953; DB 2; Length 608;
Best Local Similarity 38.1%; Pred. No. 2.2e-63;
Matches 222; Conservative 94; Mismatches 210; Indels 56; Gaps 14;

QY 60 LER-AROTPHKPEFLRDELTITVAQVDRSRNOVARALHDLHGLRQDCVALLMGNEPAY 118
DB 48 LERARLPDPNPVALDGGRRISYALFNAGWANRLARAFKAE-GVGHGSVVAAMLENRVLL 106
QY 119 WLWGLVGLKGCAMACLNINRAKSLHLCFOCCGAKVLLVSPQLQAAVEEILPSLKKDDVS 178
DB 107 AILAAALAKGAIGALVNTQGRKVLVHSLNLPKGVVEELREVEFEVHREVLGNAGH 166
QY 179 IYVYVRSNTGDSFLDKVDVESTEPIPEWSR-----EYTFSTPAL 221
DB 167 CYWD-----DG-----DTLGDGSGPPM--GWRNLMRLAQGTSENLEDTRVRLKDSCF 214
QY 222 YIYTSGLTGLPKAMITHORIW---YG-----TGLTFVSGLKADDDVITLPPHSAALLI 274
DB 215 YIYTSGLTGLPKASIMSHGK-WIKAYGGFGHSLG---GLGRDDVLYTLPCYHNNAVT 269
QY 275 GIHGCIVAGATLALRTKFSQFWDCKRYNVTYQVIGELLYLNCSPKPNDRDHKVR 334
DB 270 CWSRALAGGAAMALRRFASGFWKDVQHYRATCFYIGELCRYLLAQPCAERGNLSLT 329
QY 335 LALGNLGRDGVWRQVVRKFGDICIYEFYAATEGNIGMNYARKVAVGRVNYLQKKIITY 394
DB 330 CMIGNLRPSIWAEFKQRFQIRITEFYASSEGNIPTNFEDNTYV-----FSPATY 383
QY 395 DLIKYDVEKDEPVRDENGVCYVRPKGEVGLLVCKITQLTPNGYAGAKAQTEKKLRDVF 454
DB 384 AIVRYDLENDRPVADKAGFMKGVKGEVGLLISIAKWPFDGYTD-PAKSEAVILRDVF 442
QY 455 KKGOLYFNSGDLMM---VDHENFIYFHDVGRVDFRWKGENVATTEVADTVGLVDFVQEVN 511
DB 443 KKGDAWNTGDLMRDIGFKHTQFV---DRLGDTFRWKGENVSTTEVENALGAFDGEDAV 499
QY 512 YGVHVPDHEGRIGMAIKMENHEFDGKKLFQHADIYLPYSARPRFLRIQDTIETGTGTF 571
DB 500 YGVIEPTGTRCGMAALRLADGVLELDALAAHLDRFLPAYATPVFLRLLEVEYTTGTF 559
QY 572 KHRKMTLVEEGFNPVAKDALYFLDDTAKMVPMTEDIYNAL 613
DB 560 KYKTDLARDAYDPAVRSVKLFVRLPGSAGYQPLDAELYQAL 601

RESULT 13
ID O05307 PRELIMINARY; PRT; 597 AA.
AC O05307;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)

01-JUL-1997	(TREMBLrel. 04, Last sequence update)
01-JUN-2000	(TREMBLrel. 14, Last annotation update)
DE	HYPOTHETICAL FATTY ACID TRANSPORT PROTEIN (64.3 KDA PROTEIN).
GN	RV1206 OR MTG1364.18.
GN	Mycobacterium tuberculosis.
OC	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC	Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX	NCBI_TaxId=1773;
RP	[1]
RP	SEQUENCE FROM N.A.
RP	STRAIN=H37RV;
RC	MEDLINE=98295987; PubMed=9634230;
RA	Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.
RA	Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA	Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA	Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.
RA	Hornsby T., Jagels K., Ktogh A., McLean J., Moule S., Murphy J.,
RA	Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA	Rutter S., Seeger K., Skelton S., Squares R., Squires R., Sulston J.E.
RA	Taylor K., Whitehead S., Barrrell B.G.;
RT	"deciphering the biology of Mycobacterium tuberculosis from the
RT	complete genome sequence."
RL	Nature 393:537-544(1998).
CC	-1- FUNCTION: INVOLVED IN TRANSLLOCATION OF LONG-CHAIN FATTY ACIDS (B
CC	SIMILARITY).
CC	-1- SIMILARITY: TO OTHER ENZYMES WHICH ACT VIA AN ATP-DEPENDENT
CC	COVALENT BINDING OF AMP TO THEIR SUBSTRATE.
CC	EMBL; Z93777; CAB07829.1; -.
DR	TubercuList; RV1206; -.
DR	InterPro; IPR000873; -.
DR	Pfam; PF00501; AMP-binding; 1.
DR	PROSITE; PS00455; AMP_BINDING; 1.
KW	Hypothetical protein; Lipid transport.
SQ	SEQUENCE 597 AA; 64336 MW; A0BBE5EB19A05CB7 CRC64.

[illegible]

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::      ||||| : : : :: || | | : : : || | | : : : | : | : | :
507 TLRAGAEFGQALARYVGHLPGLYPLFRVVVGSLSLAHTTTFKSRKVLERNQAYG-ADIE 565
QY    590 DALYFLDDTAQMYPV 604
      | | | | : | | |
Db    566 DPLYVLGPDEGYVP 580

RESULT 14
O95186 PRELIMINARY; PRT; 641 AA.
ID O95186
AC O95186;
DT 01-WAY-1999 (TREMBLrel. 10, Created)
DT 01-WAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-WAY-2000 (TREMBLrel. 13, Last annotation update)
DE FATTY ACID TRANSPORT PROTEIN.
GN FATP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART;
RX MEDLINE=99096471; PubMed=9878842;
RA Fitzscher B.A., Riedel H.D., Young K.C., Streammel W.;
RT "Tissue distribution and cDNA cloning of a human fatty acid transport
RT protein (hsFAIP4).";
RL Blochim. Biophys. Acta 1443:381-385(1998).
DR EMBL; AF055899; RAD11623.1; -.
DR InterPro; IPR000566; -.
DR InterPro; IPR000873; -.
DR Pfam; PF00501; AMP-binding; 1.
DR PROSITE; PS00455; AMP-BINDING; 1.
DR PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
SQ SEQUENCE 641 AA; 71431 MW; 8C24F76C9BF81378 CRC64;
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Query Match	28.6%	Score	937	DB	4	Length	641
Best Local Similarity	36.2%	Pred. No.	3.9e-62				
Matches	231	Conservative	104	Mismatches	22	Indels	56
Gaps	15						
QY	12	LFLEPL-----LVNLCPFFQDIFGLKVAAGRRVRSYQORPARTILRAFLEKARQ	65				
DB		: : : : : : : : : : : : : : : : : : : :					
DB	29	LFELYLSGGWRFRIVFIKTRIDFGLGLVLLKVKAKVQCQLQER--RTVPILFASTVRR	86				
QY	66	TPHKPFLFGR--DETLLTAOVDRRSNOVALHDHLGRQDCVALLMGNPEAVVWLWG	123				
DB		: : : : : : : : : : : : : : : : : : : :					
DB	87	HPDKTALIFEGTDTHWTFRQDEYSVVANFLOAR--GLASGDVAIFAEMENRNEFVGLMW	145				
QY	124	LVKLGCAACLAFLNIRAKSLHLHCQCCKAGKVLIVSPELQAAVEEILPSLKDDVSIYVVS	183				
DB		: : : : : : : : : : : : : : : : : : : :					
DB	146	MAKLGEAALINTLNRDALLHCLITTSRALYFGSEMAAICEVHAS---PDPSLSLFC	202				
QY	184	RTS-----NTQDISFL-DKVEDEVSTPEIPESWRSEVTFSTPALYIYSGTTGLPKA	234				
DB		: : : : : : : : : : : : : : : : : : : :					
DB	203	SGSWEPGAAPPSTEHLLPKADKAPKHPSCP-----DKGFTDKLFYIYTSGTGLPKA	255				
QY	235	AMITHORIWTYGTLTFFVS--GLKADDYIYITLPYHSAALLIGHCIVAGATLAIKPKFS	293				
DB		: : : : : : : : : : : : : : : : : : : :					
DB	256	ALVHRSYRYRMAALYVYGFRRMRNDIVDCLPLIYHSAAGNIVIGQCLLHGMTVWIRKFS	315				
QY	294	ASQFWDDCRKYNVTIVQIGELLYRLCNSPKQPNDRDHKVRLLAINGL-----RGD	344				
DB		: : : : : : : : : : : : : : : : : : : :					
DB	316	ASRFWDDCIKYNCTIVQIGELCRYLLNQPPREAENQHQVRMALGNAGSPSGPTFFPAAS	375				
QY	345	WVRQFVKRFGDCIYEFYAATEGNIGFMNARKVAGVGRVNYLQKKIITYDLIKIYDEKD	404				
DB		: : : : : : : : : : : : : : : : : : : :					
DB	376	TYPRWLSSTGPEC-----NCSIGNEDSQVGACFNPSILFSFVYPIRLVRVNEDTM	425				
QY	405	EPVRDENGVCYVRPKGEVGLLVCKITQLTPT--FNGYAGAKAQTEKKKLDRDVFKKGDLYF	461				
DB		: : : : : : : : : : : : : : : : : : : :					
DB	426	ELIRGPQGVITPCQPGPGLVGRITQKQPLRRFDGYNLOGA--NNKKTAKDVFKKGDQAY	484				

